F. Moezie

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/068,253

DATE: 05/10/2001

TIME: 11:04:42

Input Set : A:\19624051.app

Output Set: N:\CRF3\05102001\I068253.raw

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3 <110> APPLICANT: SHIMURA, Takesada
         TORIYAMA, Satsuki
 6 <120> TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION
 8 <130> FILE REFERENCE: 146.1286
10 <140> CURRENT APPLICATION NUMBER: 09/068,253
11 <141> CURRENT FILING DATE: 1998-06-09
13 <150> PRIOR APPLICATION NUMBER: PCT/JP96/03333
14 <151> PRIOR FILING DATE: 1996-11-14
16 <150> PRIOR APPLICATION NUMBER: JP 7/322402
17 <151> PRIOR FILING DATE: 1995-11-17
19 <160> NUMBER OF SEQ ID NOS: 4
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 357
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(357)
31 <223> OTHER INFORMATION: Relevant amino acid residues in SEQ ID NO: 1 from
32
         1 to 119 in WO 95/04819
34 <300> PUBLICATION INFORMATION:
35 <301> AUTHORS: HOTTEN, Gertrud
36
         NEIDHARDT, Helge
37
         PAULISTA, Michael
38 <302> TITLE: NEW GROWTH/DIFFERENTIATION FACTOR OF THE TGF-BETA
        FAMILY
40 <310> PATENT DOC NO: WO 95/04819
41 <311> PATENT FILING DATE: 1995-02-16
42 <313> RELEVANT RESIDUES: 1 TO 119
44 <400> SEQUENCE: 1
45 cca ctg gcc act cgc cag ggc aag cga ccc agc aag aac ctt aag gct
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46 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
47
                     5
    1
                                        10
49 cgc tgc agt cgg aag gca ctg cat gtc aac ttc aag gac atg ggc tgg
                                                                      96
50 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
53 gac gac tgg atc atc gca ccc ctt gag tac gag gct ttc cac tgc gag
                                                                      144
54 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
                                40
57 ggg ctg tgc gag ttc cca ttg cgc tcc cac ctg gag ccc acg aat cat
                                                                      192
58 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
        50
                            55
61 gca gtc atc dag acc ctg atg aac tcc atg gac ccc gag tcc aca cca
62 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
                        70
                                            75
65 ccc acc tgc tgt gtg ccc acg cga ctg agt ccc atc agc atc ctc ttc
                                                                      288
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66 Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
                    85
69 att gac tot goo aac aac gtg gtg tat aag cag tat gag gac atg gtc
                                                                      336
70 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
               100
                                   105
73 gtg gag tcg tgt ggc tgc agg
                                                                      357
74 Val Glu Ser Cys Gly Cys Arg
           115
78 <210> SEQ ID NO: 2
79 <211> LENGTH: 119
80 <212> TYPE: PRT
81 <213> ORGANISM: Homo sapiens
83 <400> SEQUENCE: 2
84 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
87 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
                                    25
               20
90 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
                                40
93 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
                            55
                                                60
96 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
                        70
                                            75
99 Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
100
102 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
103
                100
                                    105
                                                        110
105 Val Glu Ser Cys Gly Cys Arg
106
            115
110 <210> SEQ ID NO: 3
111 <211> LENGTH: 27
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112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Description of Artificial Sequence:
117
        oligonucleotide
119 <220> FEATURE:
120 <221> NAME/KEY: misc_feature
121 <222> LOCATION: (1)..(27)
122 <223> OTHER INFORMATION: PCR forward primer for isolating mature-type MP52
124 <400> SEQUENCE: 3
125 ataatgccac tagcaactcg tcagggc
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128 <210> SEQ ID NO: 4
129 <211> LENGTH: 26
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Description of Artificial Sequence:
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- 137 <220> FEATURE:
- 138 <221> NAME/KEY: misc\_feature
- 139 <222> LOCATION: Complement((1)..(26))
- 140 <223> OTHER INFORMATION: PCR reverse primer for isolating mature-type MP52
- 142 <400> SEQUENCE: 4
- 143 cgtcgactac ctgcagccac acgact

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VERIFICATION SUMMARY

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Input Set : A:\19624051.app

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